



# Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2024 – 10:08 am BST

PDB ID : 8Q5D  
Title : PfrH5 bound to monoclonal antibody MAD10-466  
Authors : Farrell, B.; Higgins, M.K.  
Deposited on : 2023-08-08  
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.36.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

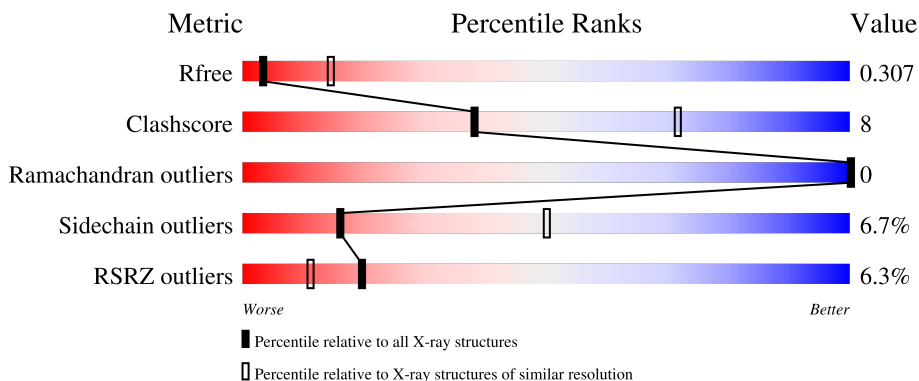
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



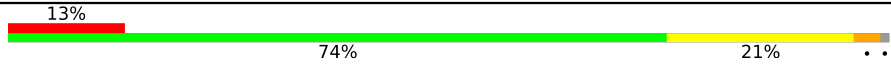
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	338	 4% 69% 14% 16%
1	D	338	 4% 66% 15% 18%
2	B	221	 71% 24% 5%
2	E	221	 9% 69% 25% 2%
3	C	215	 5% 72% 22% 3%

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Mol	Chain	Length	Quality of chain
3	F	215	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '13%', a green segment in the middle labeled '74%', and a yellow segment on the right labeled '21%'. At the far right end of the bar, there are two small black dots.</p>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11181 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PfrH5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	283	Total	C	N	O	S	0	0	0
			2406	1555	403	435	13			
1	D	278	Total	C	N	O	S	0	0	0
			2363	1525	397	428	13			

- Molecule 2 is a protein called Monoclonal antibody MAD10-466 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	211	Total	C	N	O	S	0	0	0
			1571	992	265	307	7			
2	E	213	Total	C	N	O	S	0	0	0
			1586	1001	268	310	7			

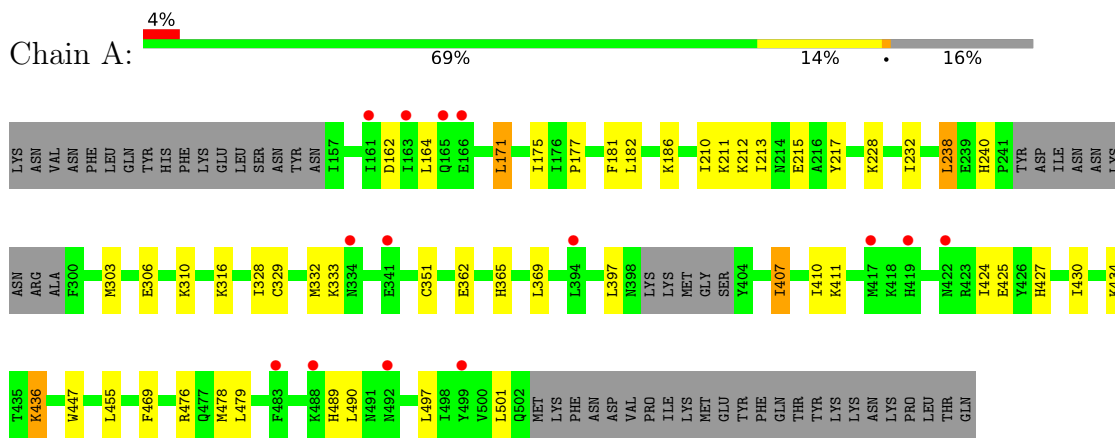
- Molecule 3 is a protein called Monoclonal antibody MAD10-466 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	210	Total	C	N	O	S	0	0	0
			1618	1009	271	333	5			
3	F	212	Total	C	N	O	S	0	0	0
			1637	1019	277	336	5			

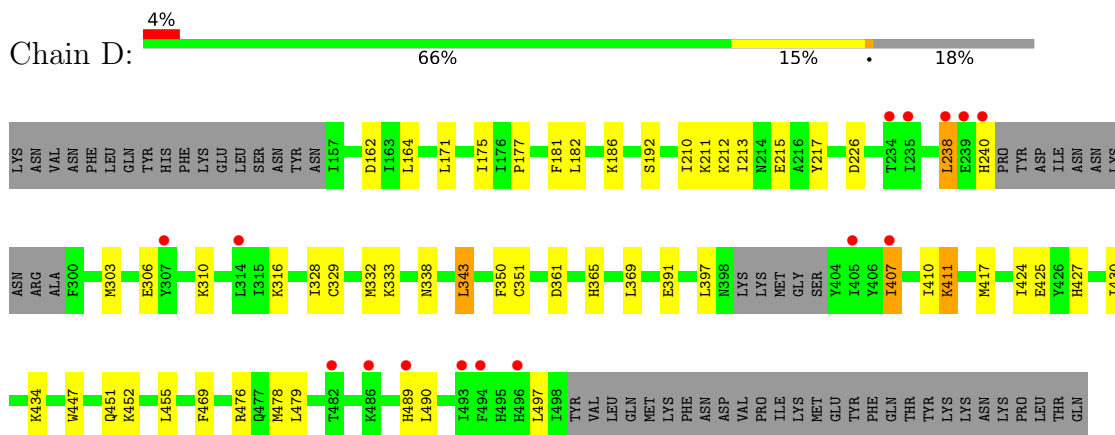
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

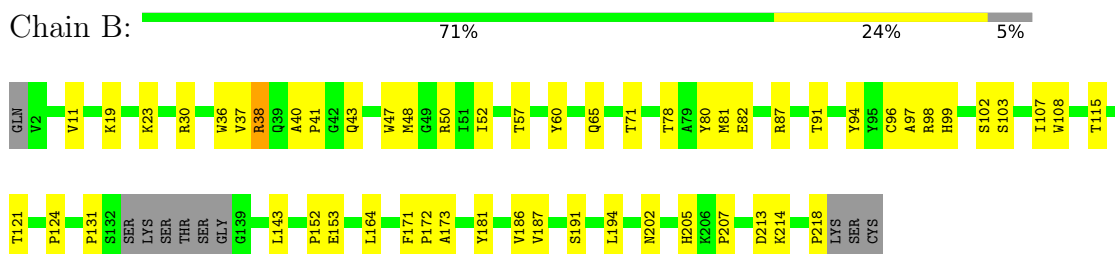
- Molecule 1: PfrH5



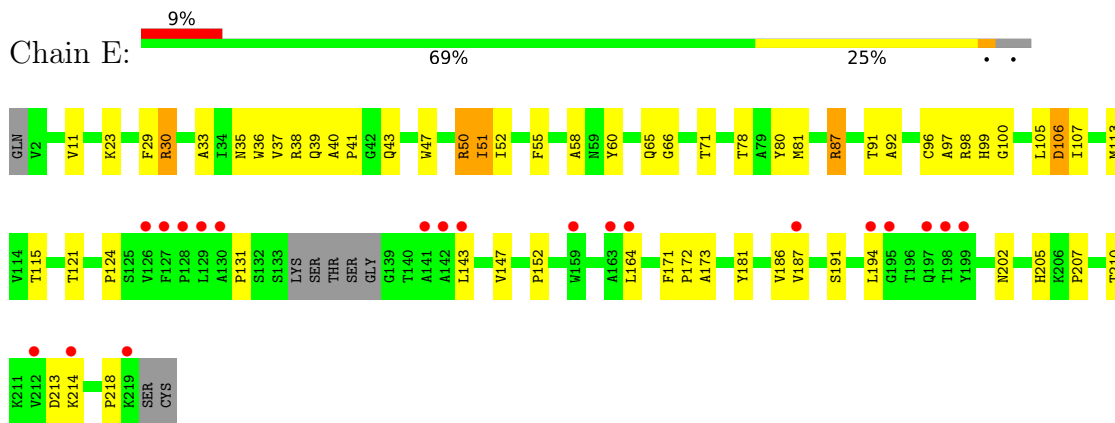
- Molecule 1: PfrH5



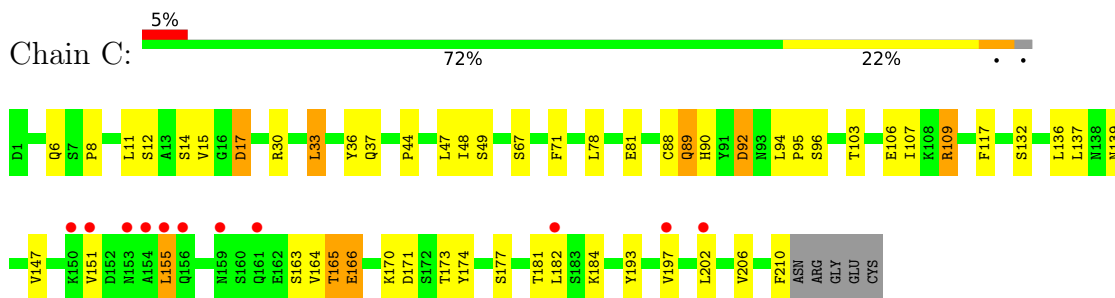
- Molecule 2: Monoclonal antibody MAD10-466 heavy chain



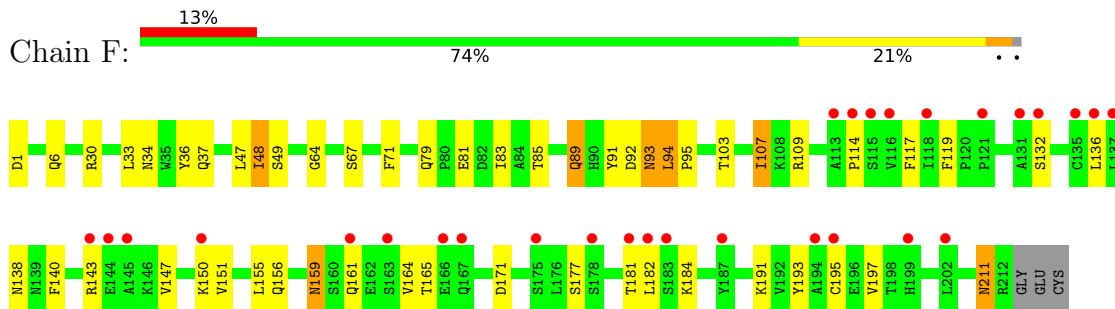
- Molecule 2: Monoclonal antibody MAD10-466 heavy chain



- Molecule 3: Monoclonal antibody MAD10-466 light chain



- Molecule 3: Monoclonal antibody MAD10-466 light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.46Å 140.41Å 83.62Å 90.00° 112.74° 90.00°	Depositor
Resolution (Å)	67.59 – 3.20 67.59 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.7 (67.59-3.20) 98.7 (67.59-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.00 (at 3.19Å)	Xtrriage
Refinement program	BUSTER 2.10.4 (26-JUL-2023)	Depositor
R, $R_{free}$	0.272 , 0.317 0.264 , 0.307	Depositor DCC
$R_{free}$ test set	1464 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.0	Xtrriage
Anisotropy	0.264	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 71.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.36$ , $\langle L^2 \rangle = 0.20$	Xtrriage
Estimated twinning fraction	0.096 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	11181	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	100.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.31	0/2456	0.51	0/3296
1	D	0.31	0/2411	0.51	0/3233
2	B	0.35	0/1607	0.59	0/2188
2	E	0.33	0/1622	0.57	0/2207
3	C	0.34	0/1654	0.58	0/2249
3	F	0.34	0/1673	0.57	0/2274
All	All	0.33	0/11423	0.55	0/15447

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2406	0	2424	28	0
1	D	2363	0	2380	30	0
2	B	1571	0	1550	36	0
2	E	1586	0	1568	37	0
3	C	1618	0	1555	32	0
3	F	1637	0	1574	25	0
All	All	11181	0	11051	168	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.



All (168) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:PHE:HB3	3:C:164:VAL:HG11	1.48	0.95
2:E:171:PHE:HB3	3:F:164:VAL:HG11	1.57	0.84
1:D:417:MET:HE1	1:D:490:LEU:HD22	1.60	0.82
2:E:40:ALA:HB3	2:E:43:GLN:HB2	1.63	0.80
1:D:238:LEU:HG	1:D:303:MET:HG3	1.66	0.77
3:C:37:GLN:HB2	3:C:47:LEU:HD11	1.69	0.75
2:B:40:ALA:HB3	2:B:43:GLN:HB2	1.72	0.72
3:C:36:TYR:HE1	3:C:89:GLN:HG2	1.54	0.70
3:F:83:ILE:HG12	3:F:107:ILE:HG13	1.75	0.69
1:D:238:LEU:HG	1:D:303:MET:CG	2.22	0.69
1:A:238:LEU:HG	1:A:303:MET:HG2	1.75	0.69
2:E:121:THR:HG22	2:E:152:PRO:HD3	1.74	0.69
3:F:150:LYS:HG2	3:F:155:LEU:HG	1.75	0.68
2:E:43:GLN:H	2:E:43:GLN:CD	1.98	0.67
2:B:38:ARG:NH1	2:B:94:TYR:OH	2.28	0.66
2:E:60:TYR:HB2	2:E:65:GLN:HG3	1.78	0.65
2:B:43:GLN:H	2:B:43:GLN:CD	1.99	0.65
2:B:60:TYR:HB2	2:B:65:GLN:HG3	1.78	0.65
3:F:164:VAL:HB	3:F:177:SER:HB3	1.80	0.64
1:A:164:LEU:HG	1:A:478:MET:HB3	1.81	0.63
2:E:173:ALA:HB1	2:E:181:TYR:HB3	1.81	0.63
3:C:164:VAL:HB	3:C:177:SER:HB3	1.80	0.63
2:B:121:THR:HG22	2:B:152:PRO:HD3	1.80	0.62
1:A:365:HIS:NE2	1:A:369:LEU:HD11	2.15	0.61
2:E:172:PRO:HG3	3:F:165:THR:HB	1.82	0.60
1:D:365:HIS:NE2	1:D:369:LEU:HD11	2.16	0.60
3:C:155:LEU:HD13	3:C:155:LEU:H	1.66	0.60
3:C:14:SER:O	3:C:17:ASP:HB2	2.03	0.59
2:B:19:LYS:HG3	2:B:82:GLU:HG3	1.84	0.59
1:A:365:HIS:CD2	2:B:30:ARG:HG2	2.38	0.59
2:E:98:ARG:HE	2:E:100:GLY:HA2	1.68	0.59
3:F:37:GLN:HB2	3:F:47:LEU:HD11	1.84	0.58
2:E:37:VAL:HG22	2:E:47:TRP:HA	1.85	0.58
2:B:99:HIS:CE1	2:B:103:SER:HA	2.39	0.58
3:C:166:GLU:HB2	3:C:174:TYR:HD1	1.69	0.57
2:B:37:VAL:HG22	2:B:47:TRP:HA	1.86	0.57
3:C:147:VAL:HG22	3:C:197:VAL:HG22	1.87	0.56
3:F:48:ILE:HG21	3:F:64:GLY:HA3	1.87	0.56
3:F:147:VAL:HG22	3:F:197:VAL:HG22	1.85	0.56
3:F:34:ASN:HD22	3:F:49:SER:HA	1.69	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:8:PRO:HG3	3:C:11:LEU:HD13	1.87	0.55
2:B:172:PRO:HG3	3:C:165:THR:HB	1.89	0.54
3:F:36:TYR:HE1	3:F:89:GLN:HG2	1.72	0.54
1:A:397:LEU:HB3	1:A:407:ILE:HD11	1.89	0.54
3:C:166:GLU:HB2	3:C:174:TYR:CD1	2.42	0.54
2:E:91:THR:HG23	2:E:115:THR:HA	1.88	0.53
2:B:23:LYS:HG2	2:B:78:THR:HG23	1.91	0.53
1:A:424:ILE:HG12	1:A:479:LEU:HB3	1.91	0.53
2:B:19:LYS:NZ	2:E:66:GLY:H	2.08	0.52
1:D:350:PHE:CD2	3:F:30:ARG:NH1	2.77	0.52
2:B:91:THR:HG23	2:B:115:THR:HA	1.91	0.51
1:A:240:HIS:NE2	1:A:489:HIS:CE1	2.79	0.51
1:D:240:HIS:NE2	1:D:489:HIS:CE1	2.78	0.51
2:E:131:PRO:HD2	2:E:218:PRO:HA	1.92	0.51
2:B:173:ALA:HB1	2:B:181:TYR:HB3	1.93	0.51
3:C:15:VAL:HG23	3:C:107:ILE:HG21	1.93	0.51
1:D:186:LYS:HG3	1:D:210:ILE:HD13	1.92	0.50
1:D:424:ILE:HG12	1:D:479:LEU:HB3	1.92	0.50
2:E:202:ASN:ND2	2:E:213:ASP:OD1	2.45	0.50
2:E:35:ASN:HB2	2:E:97:ALA:HB3	1.93	0.50
3:F:94:LEU:N	3:F:95:PRO:HA	2.26	0.50
2:E:23:LYS:HG2	2:E:78:THR:HG23	1.93	0.50
2:B:131:PRO:HD2	2:B:218:PRO:HA	1.93	0.49
1:A:181:PHE:HZ	1:A:333:LYS:HB2	1.77	0.49
1:A:182:LEU:HD21	1:A:329:CYS:HA	1.94	0.49
2:B:202:ASN:ND2	2:B:213:ASP:OD1	2.45	0.49
1:D:447:TRP:HZ3	2:E:99:HIS:CD2	2.29	0.49
3:F:114:PRO:HA	3:F:140:PHE:HB3	1.94	0.49
2:B:57:THR:HG22	2:E:55:PHE:HA	1.95	0.49
1:D:410:ILE:HG23	1:D:490:LEU:HD11	1.94	0.49
1:A:213:ILE:HG21	1:A:332:MET:HE2	1.95	0.49
2:B:97:ALA:HA	2:B:107:ILE:O	2.13	0.49
1:D:181:PHE:HZ	1:D:333:LYS:HB2	1.77	0.49
2:B:71:THR:HG23	2:B:80:TYR:HD2	1.78	0.49
2:E:164:LEU:HD21	2:E:187:VAL:HG21	1.95	0.49
3:C:15:VAL:HG22	3:C:107:ILE:HD13	1.95	0.48
2:E:186:VAL:HG21	3:F:136:LEU:HD22	1.95	0.48
1:A:410:ILE:HG23	1:A:490:LEU:HD11	1.95	0.48
3:F:191:LYS:O	3:F:211:ASN:HA	2.14	0.48
1:A:186:LYS:HG3	1:A:210:ILE:HD13	1.95	0.48
1:A:365:HIS:CD2	1:A:369:LEU:HD11	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:71:THR:HG22	2:B:82:GLU:OE1	2.14	0.48
1:D:182:LEU:HD21	1:D:329:CYS:HA	1.95	0.47
1:D:192:SER:HA	1:D:343:LEU:HD21	1.96	0.47
2:E:71:THR:HG23	2:E:80:TYR:HD2	1.78	0.47
1:A:181:PHE:CZ	1:A:333:LYS:HB2	2.49	0.47
1:A:351:CYS:HB3	1:A:455:LEU:HD22	1.96	0.47
3:C:137:LEU:HD11	3:C:147:VAL:HG21	1.96	0.47
1:A:447:TRP:HZ3	2:B:99:HIS:ND1	2.13	0.47
1:D:213:ILE:HG21	1:D:332:MET:HE2	1.97	0.47
1:D:365:HIS:CD2	1:D:369:LEU:HD11	2.49	0.47
1:A:306:GLU:HG2	1:A:310:LYS:HE2	1.97	0.46
1:D:306:GLU:HG2	1:D:310:LYS:HE2	1.98	0.46
1:D:181:PHE:CZ	1:D:333:LYS:HB2	2.50	0.46
1:D:351:CYS:HB3	1:D:455:LEU:HD22	1.97	0.46
2:E:131:PRO:HA	3:F:119:PHE:HE1	1.80	0.46
1:D:361:ASP:OD1	2:E:30:ARG:HB2	2.16	0.46
2:B:11:VAL:HB	2:B:152:PRO:HG3	1.97	0.46
3:F:6:GLN:NE2	3:F:103:THR:OG1	2.48	0.46
2:B:102:SER:HB2	3:C:49:SER:HB2	1.97	0.46
3:C:94:LEU:N	3:C:95:PRO:HA	2.30	0.46
2:B:164:LEU:HD21	2:B:187:VAL:HG21	1.97	0.45
3:C:12:SER:HA	3:C:106:GLU:O	2.16	0.45
1:D:240:HIS:NE2	1:D:489:HIS:NE2	2.64	0.45
2:E:172:PRO:CG	3:F:165:THR:HB	2.45	0.45
1:D:175:ILE:HG22	1:D:177:PRO:HD2	1.99	0.45
2:E:30:ARG:H	2:E:30:ARG:HG2	1.46	0.45
1:A:436:LYS:HE2	1:D:451:GLN:HB2	1.97	0.45
2:B:48:MET:HE1	2:B:94:TYR:HD2	1.82	0.45
2:E:39:GLN:O	2:E:92:ALA:HB1	2.17	0.45
2:E:43:GLN:CD	2:E:43:GLN:N	2.69	0.45
3:C:132:SER:HA	3:C:181:THR:HA	1.99	0.45
3:F:132:SER:HA	3:F:181:THR:HA	1.99	0.45
1:A:240:HIS:NE2	1:A:489:HIS:NE2	2.65	0.45
2:E:205:HIS:CD2	2:E:207:PRO:HD2	2.52	0.44
3:C:139:ASN:HA	3:C:173:THR:HB	1.98	0.44
3:F:79:GLN:OE1	3:F:81:GLU:OE1	2.35	0.44
1:A:175:ILE:HG22	1:A:177:PRO:HD2	2.00	0.44
2:B:205:HIS:CD2	2:B:207:PRO:HD2	2.53	0.44
3:C:92:ASP:HB3	3:C:94:LEU:HG	1.99	0.44
3:C:81:GLU:HA	3:C:170:LYS:HG2	2.00	0.44
3:C:109:ARG:HA	3:C:109:ARG:HD2	1.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:ALA:HB1	2:B:41:PRO:CD	2.49	0.43
3:C:67:SER:HA	3:C:71:PHE:CE2	2.53	0.43
1:D:217:TYR:HA	1:D:328:ILE:HD13	2.00	0.43
2:E:36:TRP:CE2	2:E:81:MET:HB2	2.54	0.43
2:B:191:SER:HA	2:B:194:LEU:HD22	2.00	0.43
2:B:124:PRO:HG3	2:B:205:HIS:HB2	2.01	0.43
3:C:6:GLN:NE2	3:C:103:THR:OG1	2.50	0.43
2:E:33:ALA:HB1	2:E:50:ARG:HD2	1.99	0.43
3:F:67:SER:HA	3:F:71:PHE:CE2	2.54	0.43
3:C:171:ASP:O	3:C:171:ASP:OD1	2.36	0.42
2:E:100:GLY:CA	2:E:106:ASP:HB2	2.49	0.42
3:C:202:LEU:HD13	3:C:206:VAL:HG22	2.01	0.42
3:C:33:LEU:HD11	3:C:88:CYS:HB2	2.01	0.42
1:D:397:LEU:HB3	1:D:407:ILE:HD11	2.01	0.42
1:D:407:ILE:HG23	1:D:411:LYS:HE3	2.02	0.42
2:E:191:SER:HA	2:E:194:LEU:HD22	2.00	0.42
2:B:102:SER:HB2	3:C:49:SER:CB	2.50	0.42
1:A:217:TYR:HA	1:A:328:ILE:HD13	2.01	0.42
2:B:36:TRP:CE2	2:B:81:MET:HB2	2.54	0.42
1:D:164:LEU:HG	1:D:478:MET:HB3	2.02	0.42
1:D:212:LYS:HA	1:D:215:GLU:HB2	2.01	0.42
1:A:447:TRP:HZ3	2:B:99:HIS:HD1	1.67	0.42
1:D:427:HIS:HA	1:D:430:ILE:HD12	2.02	0.42
2:B:19:LYS:HG3	2:B:82:GLU:CG	2.48	0.42
2:B:186:VAL:HG21	3:C:136:LEU:HD22	2.01	0.42
3:F:156:GLN:HB3	3:F:159:ASN:ND2	2.35	0.42
1:A:212:LYS:HA	1:A:215:GLU:HB2	2.02	0.41
3:F:91:TYR:CZ	3:F:93:ASN:HA	2.56	0.41
2:E:124:PRO:HD2	2:E:210:THR:HG21	2.03	0.41
2:B:108:TRP:CE3	3:C:44:PRO:HD2	2.55	0.41
3:F:151:VAL:HG13	3:F:193:TYR:CE1	2.56	0.41
1:A:228:LYS:O	1:A:232:ILE:HG13	2.20	0.41
1:A:497:LEU:HD12	1:A:501:LEU:HD22	2.02	0.41
1:A:171:LEU:HB2	1:A:232:ILE:HG12	2.02	0.41
3:C:193:TYR:HB2	3:C:210:PHE:CE1	2.55	0.41
2:E:40:ALA:HB1	2:E:41:PRO:CD	2.51	0.41
1:A:427:HIS:HA	1:A:430:ILE:HD12	2.02	0.40
3:C:151:VAL:HG13	3:C:193:TYR:CE1	2.56	0.40
1:D:424:ILE:CG1	1:D:479:LEU:HB3	2.51	0.40
2:E:87:ARG:HH11	2:E:87:ARG:HB2	1.85	0.40
2:E:124:PRO:HB2	2:E:147:VAL:HG13	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:LYS:HB3	1:D:469:PHE:HB2	2.02	0.40
3:F:147:VAL:HG13	3:F:195:CYS:HB2	2.03	0.40
2:E:51:ILE:HD12	2:E:58:ALA:HB2	2.02	0.40
1:A:434:LYS:HB3	1:A:469:PHE:HB2	2.02	0.40
2:E:11:VAL:HB	2:E:152:PRO:HG3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	277/338 (82%)	269 (97%)	8 (3%)	0	100	100
1	D	272/338 (80%)	265 (97%)	7 (3%)	0	100	100
2	B	207/221 (94%)	184 (89%)	23 (11%)	0	100	100
2	E	209/221 (95%)	187 (90%)	22 (10%)	0	100	100
3	C	208/215 (97%)	183 (88%)	25 (12%)	0	100	100
3	F	210/215 (98%)	186 (89%)	24 (11%)	0	100	100
All	All	1383/1548 (89%)	1274 (92%)	109 (8%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	274/327 (84%)	263 (96%)	11 (4%)	31	66
1	D	269/327 (82%)	254 (94%)	15 (6%)	21	57
2	B	176/185 (95%)	167 (95%)	9 (5%)	24	60
2	E	178/185 (96%)	164 (92%)	14 (8%)	12	43
3	C	187/191 (98%)	170 (91%)	17 (9%)	9	34
3	F	189/191 (99%)	170 (90%)	19 (10%)	7	29
All	All	1273/1406 (90%)	1188 (93%)	85 (7%)	16	50

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	162	ASP
1	A	171	LEU
1	A	211	LYS
1	A	238	LEU
1	A	316	LYS
1	A	362	GLU
1	A	407	ILE
1	A	411	LYS
1	A	425	GLU
1	A	436	LYS
1	A	476	ARG
2	B	38	ARG
2	B	50	ARG
2	B	52	ILE
2	B	87	ARG
2	B	96	CYS
2	B	98	ARG
2	B	143	LEU
2	B	153	GLU
2	B	214	LYS
3	C	17	ASP
3	C	30	ARG
3	C	33	LEU
3	C	48	ILE
3	C	78	LEU
3	C	89	GLN
3	C	90	HIS
3	C	92	ASP
3	C	96	SER
3	C	109	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	117	PHE
3	C	155	LEU
3	C	163	SER
3	C	165	THR
3	C	166	GLU
3	C	182	LEU
3	C	184	LYS
1	D	162	ASP
1	D	171	LEU
1	D	211	LYS
1	D	226	ASP
1	D	238	LEU
1	D	316	LYS
1	D	338	ASN
1	D	343	LEU
1	D	391	GLU
1	D	407	ILE
1	D	411	LYS
1	D	425	GLU
1	D	452	LYS
1	D	476	ARG
1	D	497	LEU
2	E	29	PHE
2	E	30	ARG
2	E	38	ARG
2	E	50	ARG
2	E	51	ILE
2	E	52	ILE
2	E	87	ARG
2	E	96	CYS
2	E	105	LEU
2	E	106	ASP
2	E	107	ILE
2	E	113	MET
2	E	143	LEU
2	E	214	LYS
3	F	1	ASP
3	F	33	LEU
3	F	48	ILE
3	F	85	THR
3	F	89	GLN
3	F	92	ASP

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Mol	Chain	Res	Type
3	F	93	ASN
3	F	94	LEU
3	F	107	ILE
3	F	109	ARG
3	F	117	PHE
3	F	138	ASN
3	F	143	ARG
3	F	159	ASN
3	F	161	GLN
3	F	171	ASP
3	F	182	LEU
3	F	184	LYS
3	F	211	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	34	ASN
3	C	89	GLN
3	F	34	ASN
3	F	89	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	283/338 (83%)	0.29	14 (4%) 29 17	65, 93, 122, 156	0
1	D	278/338 (82%)	0.34	15 (5%) 25 14	58, 92, 139, 150	0
2	B	211/221 (95%)	0.01	0 100 100	66, 86, 122, 131	0
2	E	213/221 (96%)	0.35	20 (9%) 8 4	64, 90, 157, 170	0
3	C	210/215 (97%)	0.30	11 (5%) 27 15	75, 107, 141, 148	0
3	F	212/215 (98%)	0.79	29 (13%) 3 2	62, 104, 149, 156	0
All	All	1407/1548 (90%)	0.35	89 (6%) 20 11	58, 94, 147, 170	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	150	LYS	5.6
2	E	128	PRO	5.0
2	E	194	LEU	4.8
2	E	142	ALA	4.6
3	C	154	ALA	4.3
2	E	126	VAL	4.3
3	C	151	VAL	4.2
1	D	405	ILE	4.2
2	E	143	LEU	4.1
3	F	136	LEU	3.9
3	C	156	GLN	3.9
1	D	239	GLU	3.9
2	E	199	TYR	3.8
3	F	161	GLN	3.7
1	D	496	HIS	3.6
1	D	489	HIS	3.5
3	C	155	LEU	3.5
3	F	132	SER	3.4
1	A	499	TYR	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	F	145	ALA	3.3
1	D	235	ILE	3.3
3	F	118	ILE	3.3
1	D	314	LEU	3.2
3	F	182	LEU	3.2
3	F	183	SER	3.2
2	E	214	LYS	3.1
2	E	127	PHE	3.1
3	F	116	VAL	3.1
1	D	240	HIS	3.0
3	C	153	ASN	3.0
3	C	159	ASN	3.0
3	C	202	LEU	2.9
1	A	165	GLN	2.9
3	F	144	GLU	2.8
3	F	167	GLN	2.8
3	F	137	LEU	2.8
3	F	131	ALA	2.8
3	F	114	PRO	2.8
3	F	199	HIS	2.7
1	A	492	ASN	2.7
3	F	163	SER	2.7
3	F	135	CYS	2.7
1	A	166	GLU	2.7
2	E	187	VAL	2.7
1	A	161	ILE	2.7
3	F	121	PRO	2.6
3	F	175	SER	2.6
3	F	115	SER	2.5
1	D	234	THR	2.5
2	E	219	LYS	2.5
1	A	341	GLU	2.5
2	E	198	THR	2.5
2	E	212	VAL	2.5
1	A	419	HIS	2.5
1	A	334	ASN	2.5
3	F	202	LEU	2.5
2	E	129	LEU	2.4
1	D	486	LYS	2.4
2	E	164	LEU	2.4
1	D	482	THR	2.4
3	C	197	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	488	LYS	2.4
2	E	195	GLY	2.4
3	F	166	GLU	2.3
3	F	194	ALA	2.3
2	E	159	TRP	2.3
2	E	197	GLN	2.3
2	E	163	ALA	2.3
1	D	494	PHE	2.3
3	C	150	LYS	2.3
1	D	238	LEU	2.2
2	E	141	ALA	2.2
3	F	143	ARG	2.2
1	D	307	TYR	2.2
1	A	483	PHE	2.2
1	A	163	ILE	2.2
1	A	422	ASN	2.2
1	A	394	LEU	2.1
3	F	195	CYS	2.1
1	D	493	ILE	2.1
3	F	181	THR	2.1
3	F	113	ALA	2.1
1	A	417	MET	2.0
3	F	187	TYR	2.0
3	F	178	SER	2.0
1	D	407	ILE	2.0
2	E	130	ALA	2.0
3	C	182	LEU	2.0
3	C	161	GLN	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.